1. (Original) An isolated double stranded RNA molecule comprising a first strand comprising a ribonucleotide sequence which corresponds to a nucleotide sequence of a SARS virus and a second strand comprising a ribonucleotide sequence which is complementary to said nucleotide sequence of said SARS virus, wherein said double-stranded molecule inhibits expression of said nucleotide sequence of said SARS virus.

2. (Original) The RNA molecule according to claim 1 wherein said first and second strands are separate complementary strands.

3. (Original) The RNA molecule according to claim 1 wherein said first and second strands are contained in a single molecule, wherein said single molecule comprises a loop structure.

4. (Original) The RNA molecule according to any preceding claim wherein said nucleotide sequence of a SARS virus is selected from the group consisting of an nsp1 sequence, an nsp9 sequence and a spike sequence.

5. (Currently Amended) The RNA molecule according to claim 4, wherein said first strand comprises a sequence selected from the group consisting of AACCTTTGGAGAAGATACTGT **(SEQ ID NO: 1)**, AATCACATTTGAGCTTGATGA **(SEQ ID NO: 2)**, AAGTTGCTGGTTTTGCAAAGT **(SEQ ID NO: 3)** , AAGGATGAGGAAGGCAATTTA **(SEQ ID NO: 4)**, AAGCTCCTAATTACACTCAAC **(SEQ ID NO: 5)**, and AATGTTACAGGGTTTCATACT **(SEQ ID NO: 6)**.

6. (Original) A method of detecting a SARS virus in a sample, comprising (a) contacting RNA obtained from said sample with a gene specific primer comprising a 3' region that is complementary to a SARS sequence and a 5' sequence that is not complementary to a SARS sequence and synthesizing a first strand cDNA molecule by reverse transcription followed by (b) amplifying said first strand cDNA in a PCR using a pair of primers, wherein the first primer is complementary to said 5' region of said gene specific primer and wherein the second primer comprises a sequence in the SARS genome that is upstream of the region recognized by said 3' region of said gene specific primer, and (c) detecting the product of said PCR.

7. (Original) The method of claim 6 wherein said gene specific primer is complementary to a SARS nps1, nps9 or spike sequence.

8. (Currently Amended) The method of claim 7, wherein said gene specific primer comprises a sequence is selected from the group consisting of

GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gac aac ctg ctc ata aa **(SEQ ID NO: 7)**,

GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gag gat ggg cat cag ca **(SEQ ID NO: 8)**, and

GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gtg tta aaa cca gaa gg **(SEQ ID NO: 9)**.

9. (Currently Amended) The method of claim 8, wherein said first primer comprises the sequence

GAACATCGATGACAAGCTTAGGTATCGATA **(SEQ ID NO: 10)**

10. (Currently Amended) The method of claim 6 wherein said second primer comprises a sequence selected from the group consisting of

GGG AAG TTC AAG GTT ACA AGA ATG TGA GAA **(SEQ ID NO: 11)**,

CGG TGT AAG TGC AGC CCG TCT TAC ACC GTG **(SEQ ID NO: 12)**, and

CCT TGA CCG GTG CAC CAC TTT TGA TGA TGT **(SEQ ID NO; 13)**.

11. (Original) A method of treating or preventing a coronavirus infection in a subject, comprising administering to said subject and effective amount of a composition comprising an isolated double stranded RNA molecule, wherein said RNA molecule comprises a first strand comprising a ribonucleotide sequence which corresponds to a nucleotide sequence of a coronavirus and a second strand comprising a ribonucleotide sequence which is complementary to said nucleotide sequence of said coronavirus, wherein said double-stranded molecule inhibits expression of said nucleotide sequence of said coronavirus.

12. (Original) The method according to claim 11, wherein said coronavirus is a SARS virus.

13. (Original) The method according to claim 12, wherein said first and second strands are separate complementary strands.

14. (Original) The method according to claim 12, wherein said first and second strands are contained in a single molecule, wherein said single molecule comprises a loop structure.

15. (Currently Amended) The method according to ~~any of claims 12-13~~ **claim 12** wherein said nucleotide sequence of a SARS virus is selected from the group consisting of an nsp1 sequence, an nsp9 sequence and a spike sequence.

16. (Currently Amended) The method according to claim 15, wherein said first strand comprises a sequence selected from the group consisting of AACCTTTGGAGAAGATACTGT **(SEQ ID NO: 1)**, AATCACATTTGAGCTTGATGA **(SEQ ID NO: 2)**, AAGTTGCTGGTTTTGCAAAGT **(SEQ ID NO: 3)**, AAGGATGAGGAAGGCAATTTA **(SEQ ID NO: 4)**, AAGCTCCTAATTACACTCAAC **(SEQ ID NO: 5)**, and AATGTTACAGGGTTTCATACT **(SEQ ID NO: 6)**.

17. (Original) The method according to claim 15 wherein said double stranded RNA molecule comprises a sequence selected from the group consisting of SC2, SC5, SC14 and SC15.

18. (Original) The method according to claim 12, wherein said double stranded RNA molecule is delivered into the airway of said subject.

19. (Original) The method according to claim 18, wherein said delivery into said airway is achieved by intranasal delivery or by delivery into the trachea.

20. (Original) The method according to claim 12, wherein said composition comprises said double stranded RNA molecule in a carrier comprising an aqueous glucose solution free of RNAse.

21. (Original) The method according to claim 20 wherein said glucose solution comprises about 5% glucose.

22. (Original) The method according to claim 12, wherein the dosage of said double stranded RNA molecule is 1-100 mg per kg of body weight of said subject.

23. (Original) The method according to claim 12, wherein said composition is delivered as an aqueous RNA-free solution, in an aerosol or in a powder.

24. (Original) A method of treating a respiratory disease in a subject, comprising administering to the airway of said subject a double stranded RNA molecule comprising a first strand comprising a ribonucleotide sequence which corresponds to a nucleotide sequence of a gene implicated in said disease and a second strand comprising a ribonucleotide sequence which is complementary to said nucleotide sequence of said nucleotide sequence of said gene, wherein said gene implicated in said disease exhibits undesirably high levels of gene expression in said disease, and wherein said double-stranded molecule inhibits expression of said nucleotide sequence of said gene implicated in said disease.

25. (Original) The method according to claim 24, wherein said gene implicated in said disease is a gene of a pathogenic organism.

26. (Original) The method according to claim 25, wherein said pathogenic organism is a bacterium, a virus or a fungus.

27. (Original) The method according to claim 24, wherein said disease is autoimmune inflammation or lung cancer.

28. (Original) The method according to claim 12, wherein at least two double stranded RNA molecules targeting at least two different nucleotide sequences of a SARS virus are used.

29. (Original) The method according to claim 28 wherein said two nucleotide sequences are selected from the group consisting of an nsp1 sequence, an nsp9 sequence and a spike sequence.